1
SEQUENCE LISTING

<110> Shaaltiel, Yoseph
       Baum, Gideon
       Sharon Hashmueli
       Ayala Lewkowicz
       Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<160> 14

<170> PatentIn version 3.3

<210> 1
<211> 22
<212> PRT
<213> Artificial sequence

<220>
<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1   5   10   15

Leu Ser Ser Ala Glu Phe
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<210> 2
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met
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<210> 3
<211> 21
<212> DNA
<213> Artificial sequence

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<223> Single strand DNA oligonucleotide

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cagaattcgc ccgcccctgc a   21

<210> 4
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<212> DNA
<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

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ctcagatctt ggcgatgcca ca   22

<210> 5
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<212> DNA

<213> Artificial sequence

<220>
<223> Single strand DNA oligonucleotide

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ctcagaagac cagagggct   19

<210> 6
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caaagcggcc atcgtgc   17

<210> 7
<211> 1491
<212> DNA
<213> Homo sapiens

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acatactgtg actcctttga cccccgacc tttcctgccc ttggtacctt cagccgctat   120

gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatcac   180

acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga   240

tttggagggg ccatgacaga tgctgctgct ctcaacatcc ttgccctgtc accccctgcc   300

caaaatttgc tacttaaatc gtacttctct gaagaaggaa tcggatataa catcatccgg   360

gtacccatgg ccagctgtga cttctccatc cgcacctaca cctatgcaga caccccctgat   420

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attcaccgag ccctgcagtt ggcccagcgt cccgtttcac tccttgccag ccccctggaca   540

tcacccactt ggctcaagac caatggagcg gtgaatggga aggggtcact caagggacag   600

cccggagaca tctaccacca gacctgggcc agatactttg tgaagttcct ggatgcctat   660

gctgagcaca agttacagtt ctgggcagtg acagctgaaa atgagccttc tgctgggctg   720

ttgagtggat accccttcca gtgcctgggc ttcaccccctg aacatcagcg agacttcatt   780

gcccgtgacc taggtcctac cctcgccaac agtactcacc acaatgtccg cctactcatg   840

ctggatgacc aacgcttgct gctgccccac tgggcaaagg tggtactgac agacccagaa   900

gcagctaaat atgttcatgg cattgctgta cattggtacc tggactttct ggctccagcc   960

aaagccaccc taggggagac acaccgcctg ttccccaaca ccatgctctt tgcctcagag   1020

gcctgtgtgg gctccaagtt ctgggagcag agtgtgcggc taggctcctg ggatcgaggg   1080

atgcagtaca gccacagcat catcacgaac ctcctgtacc atgtggtcgg ctggaccgac   1140

tggaaccttg ccctgaaccc cgaaggagga cccaattggg tgcgtaactt tgtcgacagt   1200

cccatcattg tagacatcac caaggacacg ttttacaaac agcccatgtt ctaccacctt   1260

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aagaacgacc tggacgcagt ggcactgatg catcccgatg gctctgctgt tgtggtcgtg   1380

ctaaaccgct cctctaagga tgtgcctctt accatcaagg atcctgctgt gggcttcctg   1440

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<210> 8
<211> 335
<212> PRT
<213> Homo sapiens

<400> 8

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
1   5   10   15

Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
            20   25   30

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        35   40   45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
        50   55   60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
65   70   75   80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
                85   90   95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
            100   105   110

Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His
        115   120   125

Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His
    130   135   140

Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala
145   150   155   160

Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala
                165   170   175

Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu
            180   185   190

Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
        195   200   205

Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn
    210   215   220

Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile
225   230   235   240

Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr

```
                 245                    250                    255

His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg Val
            260                 265                 270


Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu Met
        275                 280                 285


His Pro Asp Gly Ser Ala Val Val Val Leu Asn Arg Ser Ser Lys
    290                 295                 300


Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr
305                 310                 315                 320


Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
                325                 330                 335
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<210>   9
<211>   338
<212>   DNA
<213>   Cauliflower mosaic virus

<400>   9
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ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg accccacccc     180

acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga     240

tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct     300

tcctctatat aaggaagttc atttcatttg gagaggac                             338
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<210>   10
<211>   66
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Nucleic acid sequence encoding the ER signal peptide

<400>   10
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gaattc                                                                66
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<210>   11
<211>   21
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Nucleic acid sequence encoding the vacuolar targeting sequence

<400>   11
gatcttttag tcgatactat g                                               21
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<210>   12
<211>   167
<212>   DNA
<213>   Artificial sequence
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<220>
<223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>
<221> misc_feature
<222> (162)..(162)
<223> n is a, c, g, or t

<400> 12
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agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg   120

tttataataa acaaagactt tgtcccaaaa acccccccccc cngcaga   167

<210> 13
<211> 2186
<212> DNA
<213> Artificial sequence

<220>
<223> nucleic acid sequence encoding high mannose human
       glucocerebrosidase (GCD)

<220>
<221> misc_feature
<222> (2181)..(2181)
<223> n is a, c, g, or t

<400> 13
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ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa   120

ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg accccccaccc   180

acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga   240

tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct   300

tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac   360

aattaccaac aacaacaaac aacaaacaac attacaatta ctatttacaa ttacagtcga   420

gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt   480

ctcctatcat tatcctcggc cgaattcgcc cgcccctgca tccctaaaag cttcggctac   540

agctcggtgg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgacctttt   600

cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg   660

agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca   720

gaacagaagt tccagaaagt gaagggattt ggaggggcca tgacagatgc tgctgctctc   780

aacatccttg ccctgtcacc ccctgcccaa aatttgctac ttaaatcgta cttctctgaa   840

gaaggaatcg gatataacat catccgggta cccatggcca gctgtgactt ctccatccgc   900

acctacacct atgcagacac ccctgatgat ttccagttgc acaacttcag cctcccagag   960

gaagatacca agctcaagat acccctgatt caccgagccc tgcagttggc ccagcgtccc   1020

gtttcactcc ttgccagccc ctggacatca cccacttggc tcaagaccaa tggagcggtg   1080

aatgggaagg ggtcactcaa gggacagccc ggagacatct accaccagac ctgggccaga   1140

tactttgtga gttcctggat gcctatgct gagcacaagt tacagttctg ggcagtgaca   1200

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gctgaaaatg agccttctgc tgggctgttg agtggatacc ccttccagtg cctgggcttc   1260

acccctgaac atcagcgaga cttcattgcc cgtgacctag gtcctaccct cgccaacagt   1320

actcaccaca atgtccgcct actcatgctg gatgaccaac gcttgctgct gccccactgg   1380

gcaaaggtgg tactgacaga cccagaagca gctaaatatg ttcatggcat tgctgtacat   1440

tggtacctgg actttctggc tccagccaaa gccaccctag gggagacaca ccgcctgttc   1500

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gtgcggctag gctcctggga tcgagggatg cagtacagcc acagcatcat cacgaacctc   1620

ctgtaccatg tggtcggctg gaccgactgg aaccttgccc tgaaccccga aggaggaccc   1680

aattgggtgc gtaactttgt cgacagtccc atcattgtag acatcaccaa ggacacgttt   1740

tacaaacagc ccatgttcta ccaccttggc cacttcagca gttcattcc tgagggctcc   1800

cagagagtgg ggctggttgc cagtcagaag aacgacctgg acgcagtggc actgatgcat   1860

cccgatggct ctgctgttgt ggtcgtgcta aaccgctcct ctaaggatgt gcctcttacc   1920

atcaaggatc ctgctgtggg cttcctggag acaatctcac ctggctactc cattcacacc   1980

tacctgtggc atcgccaaga tcttttagtc gatactatgt aatttcatga tctgtttgt   2040

tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga   2100

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gtcccaaaaa ccccccccc ngcaga                                          2186
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<210>  14
<211>  526
<212>  PRT
<213>  Artificial sequence

<220>
<223>  High mannose human glucocerebrosidase (GCD)

<400>  14

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1               5                   10                  15


Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
            20                  25                  30


Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
        35                  40                  45


Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
    50                  55                  60


Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
65                  70                  75                  80


Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
                85                  90                  95


Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
            100                 105                 110
```

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
  115   120   125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
130   135   140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
145   150   155   160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
     165   170   175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
    180   185   190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
  195   200   205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
  210   215   220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
225   230   235   240

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
    245   250   255

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
  260   265   270

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
  275   280   285

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
  290   295   300

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
305   310   315   320

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
    325   330   335

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
  340   345   350

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
  355   360   365

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
  370   375   380

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
385   390   395   400

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
  405   410   415

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Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
        420             425             430

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
        435             440             445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
    450             455             460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
465             470             475             480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
            485             490             495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
        500             505             510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
        515             520             525
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